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1009
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,795

DATE: 11/20/2001

TIME: 11:01:30

Input Set : N:\Crf3\RULE60\09840795.txt

Output Set: N:\CRF3\11202001\I840795.raw

3 <110> APPLICANT: Murphy, Erin E.
4 Mattson, Jeanine D.
5 Bates, Elizabeth Esther Mary
6 Gorman, Daniel M.
7 Lebecque, Serge J.E.
9 <120> TITLE OF INVENTION: Mammalian Genes; Related Reagents
11 <130> FILE REFERENCE: SF0818K
13 <140> CURRENT APPLICATION NUMBER: 09/840,795
14 <141> CURRENT FILING DATE: 2001-04-23
15 <150> PRIOR APPLICATION NUMBER: 09/351,777
16 <151> PRIOR FILING DATE: 1999-07-12
W--> 17 <160> NUMBER OF SEQ ID: 19
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1137
23 <212> TYPE: DNA
24 <213> ORGANISM: primate
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (99)..(998)
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31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (367)
33 <223> OTHER INFORMATION: W; may be A or T
35 <220> FEATURE:
36 <221> NAME/KEY: mat_peptide
37 <222> LOCATION: (132)..(998)
39 <400> SEQUENCE: 1
40 cgcaggcgga cggggggcaa aggaggtggc atgtcgggtca ggcacagcag ggtcctgtgt 60
42 ccgcgctgag ccgcgctctc cctgctccag caaggacc atg agg gcg ctg gag ggg 116
43 Met Arg Ala Leu Glu Gly
44 -10
46 cca ggc ctg tcg ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg 164
47 Pro Gly Leu Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu
48 -5 -1 1 5 10
50 ccg gtg ccg gct gta cgc gga gtg gca gaa aca ccc acc tac ccc tgg 212
51 Pro Val Pro Ala Val Arg Gly Val Ala Glu Thr Pro Thr Tyr Pro Trp
52 15 20 25
54 cgg gac gca gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca 260
55 Arg Asp Ala Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro
56 30 35 40
58 ggc acc ttt gtg cag cgg ccg tgc cgc cga gac agc ccc atg acg tgt 308
59 Gly Thr Phe Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Met Thr Cys
60 45 50 55
62 ggc ccg tgt cca ccg cgc cac tac acg cag ttc tgg aac tac ctg gag 356
63 Gly Pro Cys Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu
64 60 65 70 75

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66 cgc tgc cgc twc tgc tac gtc ctc tgc ggg gag cgt gag gag gag gca 404
W--> 67 Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly Glu Arg Glu Glu Glu Ala
68                               80                               85                               90
70 cgg gct tgc cac gcc acc cac aac cgt gcc tgc cgc tgc cgc acc ggc 452
71 Arg Ala Cys His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly
72                               95                               100                               105
74 ttc ttc gcg cac gct ggt ttc tgc ttg gag cac gca tcg tgt cca cct 500
75 Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro
76                               110                               115                               120
78 ggt gcc ggc gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc 548
79 Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
80                               125                               130                               135
82 cag ccg tgc ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag 596
83 Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu
84 140                               145                               150                               155
86 cag tgc cag ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc aat 644
87 Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Asn
88                               160                               165                               170
90 gtg cca ggc tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc 692
91 Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly
92                               175                               180                               185
94 ttc ccc ctc agc acc agg gta cca gga gct gag gag tgt gag cgt gcc 740
95 Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala
96                               190                               195                               200
98 gtc atc gac ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag 788
99 Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln
100                               205                               210                               215
102 cgg ctg ctg cag gcc ctc gag gcc ccg gag ggc tgg ggt ccg aca cca 836
103 Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu Gly Trp Gly Pro Thr Pro
104 220                               225                               230                               235
106 agg gcg ggc cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg 884
107 Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr
108                               240                               245                               250
110 gag ctc ctg ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag 932
111 Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln
112                               255                               260                               265
114 gcg ctg cgc gtg gcc agg atg ccc ggg ctg gag cgg agc gtc cgt gag 980
115 Ala Leu Arg Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu
116                               270                               275                               280
118 cgc ttc ctc cct gtg cac tgatcctggc cccctcttat ttattctaca 1028
119 Arg Phe Leu Pro Val His
120                               285
122 tccttggcac cccacttgca ctgaaagagg ctttttttta aatagaagaa atgaggtttc 1088
124 ttaaagctta tttttataaa gctttttcat aaaaaaaaaa aaaaaaaaaa 1137
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 300
129 <212> TYPE: PRT
130 <213> ORGANISM: primate
132 <220> FEATURE:

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Input Set : N:\Crf3\RULE60\09840795.txt

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133 <221> NAME/KEY: misc_feature
 134 <222> LOCATION: (79)
 135 <223> OTHER INFORMATION: Xaa at residue 79 is undetermined.
 138 <400> SEQUENCE: 2
 139 Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val Leu
 140 -10 -5 -1 1 5
 142 Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
 143 10 15 20
 145 Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
 146 25 30 35
 148 Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
 149 40 45 50
 151 Asp Ser Pro Met Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
 152 55 60 65
 W--> 154 Phe Trp Asn Tyr Leu Glu Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly
 155 70 75 80 85
 157 Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
 158 90 95 100
 160 Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
 161 105 110 115
 163 His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
 164 120 125 130
 166 Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
 167 135 140 145
 169 Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
 170 150 155 160 165
 172 Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
 173 170 175 180
 175 Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
 176 185 190 195
 178 Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
 179 200 205 210
 181 Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
 182 215 220 225
 184 Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
 185 230 235 240 245
 187 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
 188 250 255 260
 190 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
 191 265 270 275
 193 Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
 194 280 285
 197 <210> SEQ ID NO: 3
 198 <211> LENGTH: 1031
 199 <212> TYPE: DNA
 200 <213> ORGANISM: primate
 202 <220> FEATURE:
 203 <221> NAME/KEY: CDS
 204 <222> LOCATION: (402)..(1031)

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Input Set : N:\Crf3\RULE60\09840795.txt

Output Set: N:\CRF3\11202001\I840795.raw

206 <220> FEATURE:
 207 <221> NAME/KEY: mat_peptide
 208 <222> LOCATION: (525)..(1031)
 210 <220> FEATURE:
 211 <221> NAME/KEY: misc_feature
 212 <222> LOCATION: (2)
 213 <223> OTHER INFORMATION: n; may be A, C, G, or T
 215 <220> FEATURE:
 216 <221> NAME/KEY: misc_feature
 217 <222> LOCATION: (9)
 218 <223> OTHER INFORMATION: n; may be A, C, G, or T
 220 <220> FEATURE:
 221 <221> NAME/KEY: misc_feature
 222 <222> LOCATION: (664)
 223 <223> OTHER INFORMATION: k; may be G or T
 225 <220> FEATURE:
 226 <221> NAME/KEY: misc_feature
 227 <222> LOCATION: (956)
 228 <223> OTHER INFORMATION: n; may be A, C, G, or T
 230 <220> FEATURE:
 231 <221> NAME/KEY: misc_feature
 232 <222> LOCATION: (989)
 233 <223> OTHER INFORMATION: n; may be A, C, G, or T
 235 <400> SEQUENCE: 3

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 238 aagcttcgct atgggaagtc gttcctttgc tctctcgcc ccagtcctcc tccctgggtc 120
 240 tccctcagccg ctgtcggagg agagcaccg gagacgcggg ctgcagtcgc ggcggcttct 180
 242 ccccgccctgg gcggccgcgc cgctgggacg gtgctgagcg cccctagagc ctcccttgcc 240
 244 gcctccctcc tctgcccggc cgcagcagtg cacatggggg gttggaggta gatgggctcc 300
 246 cggcccggga ggccggcgtg gatgcggcgc tgggcagaag cagccgccga ttccagctgc 360
 248 cccgcgcgcc ccgggcgcc ctgcgagtc ccggttcagc c atg ggg acc tct ccg 416
 249 Met Gly Thr Ser Pro
 250 -40
 252 agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc cga gcc 464
 253 Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg Arg Ala
 254 -35 -30 -25
 256 aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc ctt agc 512
 257 Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe Leu Ser
 258 -20 -15 -10 -5
 260 acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att ggc aca 560
 261 Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile Gly Thr
 262 -1 1 5 10
 264 tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt gac aag 608
 265 Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys Asp Lys
 266 15 20 25
 268 tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca agc tgc 656
 269 Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr Ser Cys
 270 30 35 40
 272 gcg tct gkc agc agt tgc cct gtg ggg acc ttt acc agg cat gag aat 704

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W--> 273 Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn
      274 45          50          55          60
      276 ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg cca atg 752
      277 Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met
      278          65          70          75
      280 att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc act tgc 800
      281 Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys
      282          80          85          90
      284 cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat acg gtg 848
      285 Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val
      286          95          100          105
      288 tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act gag gat 896
      289 Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp
      290          110          115          120
      292 gtg cgg tgt aag cag tgt gct cgg ggg tac ttc tca gat gtg cct tct 944
      293 Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe Ser Asp Val Pro Ser
      294 125          130          135          140
W--> 296 agt gtg atg aan gca aag cat aca cag act gtc tgg atc aga acn tgg 992
W--> 297 Ser Val Met Xaa Ala Lys His Thr Gln Thr Val Trp Ile Arg Xaa Trp
      298          145          150          155
      300 ttg gtg atc aag ccg ggg gga cca agg aga cag aca act 1031
      301 Leu Val Ile Lys Pro Gly Gly Pro Arg Arg Gln Thr Thr
      302          160          165
      305 <210> SEQ ID NO: 4
      306 <211> LENGTH: 210
      307 <212> TYPE: PRT
      308 <213> ORGANISM: primate
      310 <220> FEATURE:
      311 <221> NAME/KEY: misc_feature
      312 <222> LOCATION: (47)
      313 <223> OTHER INFORMATION: Xaa at residue 47 is undetermined.
      315 <220> FEATURE:
      316 <221> NAME/KEY: misc_feature
      317 <222> LOCATION: (144)
      318 <223> OTHER INFORMATION: Xaa at residue 144 is undetermined.
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      321 <221> NAME/KEY: misc_feature
      322 <222> LOCATION: (155)
      323 <223> OTHER INFORMATION: Xaa at residue 155 is undetermined.
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      330 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
      331 -25 -20 -15 -10
      333 Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
      334 -5 -1 1 5
      336 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
      337 10 15 20
      339 Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09840795.txt

Output Set: N:\CRF3\11202001\I840795.raw

L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18